



ST00004 US DIV Sequence Listing.txt
SEQUENCE LISTING

<110> Maudy, Isabella
Mercken, Luc
Fournier, Alain

<120> Partners of the PTB1 Domain of FE65, Preparation and Uses

<130> ST00004-US

<140> 09/780,996

<141> 2001-02-09

<150> FR00/01628

<151> 2000-02-10

<150> US 60/198,500

<151> 2000-04-18

<160> 11

<170> PatentIn version 3.2

<210> 1

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1

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gagatgaccg aggaggagct ggccctgga cgcagcagtg tggcagtcaa caattgcattc 120

cgtcagctct cttaccacaa aaacaacctg catgacccca tgtctggggg ctggggggaa 180

ggaaaggatc tgctactgca gctggaggat gagacactaa agctagtggc gccacagagc 240

caggcactgc tgcacgcccc acccatcatc agcatccgcg tgtggggcgt cgggcgggac 300

agtggaaaggc actttgccta cgtagctcgat gataagctga cccagatgct caagtgccac 360

gtgtttcgct gtgaggcacc tgccaagaac atcgccacca gcctgcatga gatctgctct 420

aagatcatgg ccgaacggcg taatgcc 447

<210> 2

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2

Pro Pro Arg Asn Thr Asn Pro Gly Ile Lys Cys Phe Ala Val Arg Ser
1 5 10 15

Leu Gly Trp Val Glu Met Thr Glu Glu Glu Leu Ala Pro Gly Arg Ser
20 25 30

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Ser Val Ala Val Asn Asn Cys Ile Arg Gln Leu Ser Tyr His Lys Asn
35 40 45

Asn Leu His Asp Pro Met Ser Gly Gly Trp Gly Glu Gly Lys Asp Leu
50 55 60

Leu Leu Gln Leu Glu Asp Glu Thr Leu Lys Leu Val Glu Pro Gln Ser
65 70 75 80

Gln Ala Leu Leu His Ala Gln Pro Ile Ile Ser Ile Arg Val Trp Gly
85 90 95

Val Gly Arg Asp Ser Gly Arg Asp Phe Ala Tyr Val Ala Arg Asp Lys
100 105 110

Leu Thr Gln Met Leu Lys Cys His Val Phe Arg Cys Glu Ala Pro Ala
115 120 125

Lys Asn Ile Ala Thr Ser Leu His Glu Ile Cys Ser Lys Ile Met Ala
130 135 140

Glu Arg Arg Asn Ala
145

<210> 3
<211> 28
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 3
cttcccggtt ccccacgga ataccaac

28

<210> 4
<211> 27
<212> DNA
<213> Artificial

<220>
<223> PCR primer

<400> 4
ggggtcgacg gcattacgcc gttccgc

27

<210> 5

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<211> 18
<212> DNA
<213> Artificial

<220>
<223> GAL4TA oligonucleotide

<400> 5
ccactacaat ggatgatg

18

<210> 6
<211> 1047
<212> DNA
<213> Homo sapiens

<400> 6
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cacccagctt ttgtcaacta ctctaccagc cagaagatct cccgcctgg ggactcgat 120
gactcccgga gcgtgaacag tgtgcttctc tttaccatcc tgaacccat ttattcgatc 180
accacggatg ttctttacac tatctgtaat ctttgtggcc ctgtccagag aattgtcatt 240
ttcaggaaga atggagttca ggcgatggtg gaatttgact cagttcaaag tgcccagcgg 300
gccaaggcct ctctcaatgg ggctgatatac tattctggct gttgcactct gaagatcgaa 360
tacgcaaagc ctacacgctt gaatgtgttc aagaatgatc aggatacttg ggactacaca 420
aaccccaatc tcagtgacca aggtgaccct ggcagcaacc ccaacaaacg ccagaggcag 480
ccccctctcc tgggagatca ccccgacaa tatggaggc cccacggctgg gtaccacagc 540
cattaccatg atgagggcta cggggccccc ccacctcaact acgaagggag aaggatgggt 600
ccaccagtgg ggggtcaccc tcggggccca agtcgctacg gccccagta tgggcacccc 660
ccacccccc ccccacccacc cgagtatggc cctcacgccc acagccctgt gctcatggc 720
tatggcttgg atcaatctaa gatgaactgt gaccgagtct tcaatgtctt ctgcttatat 780
ggcaatgtgg agaaggtgaa attcatgaaa agcaagccgg gggccgccat ggtggagatg 840
gctgatggct acgctgtaga cggggccatt acccacctca acaacaactt catgttggg 900
cagaagctga atgtctgtgt ctccaaggcag ccagccatca tgccctggta gtcatacggg 960
ttggaagacg ggtcttgcag ttacaaagac ttcagtgaat cccgaaacaa tcggttctcc 1020
accccaagacg aggcagccaa gaaccgc 1047

<210> 7
<211> 349
<212> PRT
<213> Homo sapiens

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<400> 7

Val Leu Gly Ala Cys Asn Ala Val Asn Tyr Ala Ala Asp Asn Gln Ile
1 5 10 15

Tyr Ile Ala Gly His Pro Ala Phe Val Asn Tyr Ser Thr Ser Gln Lys
20 25 30

Ile Ser Arg Pro Gly Asp Ser Asp Asp Ser Arg Ser Val Asn Ser Val
35 40 45

Leu Leu Phe Thr Ile Leu Asn Pro Ile Tyr Ser Ile Thr Thr Asp Val
50 55 60

Leu Tyr Thr Ile Cys Asn Pro Cys Gly Pro Val Gln Arg Ile Val Ile
65 70 75 80

Phe Arg Lys Asn Gly Val Gln Ala Met Val Glu Phe Asp Ser Val Gln
85 90 95

Ser Ala Gln Arg Ala Lys Ala Ser Leu Asn Gly Ala Asp Ile Tyr Ser
100 105 110

Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Lys Pro Thr Arg Leu Asn
115 120 125

Val Phe Lys Asn Asp Gln Asp Thr Trp Asp Tyr Thr Asn Pro Asn Leu
130 135 140

Ser Gly Gln Gly Asp Pro Gly Ser Asn Pro Asn Lys Arg Gln Arg Gln
145 150 155 160

Pro Pro Leu Leu Gly Asp His Pro Ala Glu Tyr Gly Pro His Gly
165 170 175

Gly Tyr His Ser His Tyr His Asp Glu Gly Tyr Gly Pro Pro Pro Pro
180 185 190

His Tyr Glu Gly Arg Arg Met Gly Pro Pro Val Gly Gly His Arg Arg
195 200 205

Gly Pro Ser Arg Tyr Gly Pro Gln Tyr Gly His Pro Pro Pro Pro Pro
210 215 220

Pro Pro Pro Glu Tyr Gly Pro His Ala Asp Ser Pro Val Leu Met Val

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225 230 235 240

Tyr Gly Leu Asp Gln Ser Lys Met Asn Cys Asp Arg Val Phe Asn Val
245 250 255Phe Cys Leu Tyr Gly Asn Val Glu Lys Val Lys Phe Met Lys Ser Lys
260 265 270Pro Gly Ala Ala Met Val Glu Met Ala Asp Gly Tyr Ala Val Asp Arg
275 280 285Ala Ile Thr His Leu Asn Asn Asn Phe Met Phe Gly Gln Lys Leu Asn
290 295 300Val Cys Val Ser Lys Gln Pro Ala Ile Met Pro Gly Gln Ser Tyr Gly
305 310 315 320Leu Glu Asp Gly Ser Cys Ser Tyr Lys Asp Phe Ser Glu Ser Arg Asn
325 330 335Asn Arg Phe Ser Thr Pro Glu Gln Ala Ala Lys Asn Arg
340 345

<210> 8
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> n= a or g or c or t/u

<220>
<221> misc_feature
<222> (914)..(914)
<223> n is a, c, g, or t

<400> 8
cggggggatg tggatgatgc tgggactgt tctggggcca ggtataatga ctggtctgat 60
gatgatgatg acagcaatga gagcaagagt atagtatggt acccaccttg ggctcggtt 120
gggactgaag ctggaaccag agctagggcc agggcaaggg ccagggctac ccgggcacgt 180
cgggctgtcc agaaacgggc ttcccccaat tcagatgata ccgtttgtc ccctcaagag 240
ctacaaaagg ttctttgctt ggtttagatg tctgaaaagc cttatattct tgaagcagct 300
ttaattgctc tggtaacaa tgctgcttat gcatttaaca gagatattat tcgtgatctg 360

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ggtgtctcc	caattgtcgc	aaagattctc	aatactcggt	atcccatagt	taaggaaaag	420
gcttaattg	tcctgaataa	cttgagtgtg	aatgctgaaa	atcagcgcag	gcttaaagta	480
tacatgaatc	aagtgtgtga	tgacacaatc	acttctcgct	tgaactcatc	tgtgcagctt	540
gctggactga	gattgcttac	aaatatgact	gttactaatg	agtatcagca	catgcttgct	600
aattccattt	ctgacttttt	tcgttattt	tcagcgggaa	atgaagaaac	caaacttcag	660
gttctgaaac	tcctttgaa	tttggctgaa	aatccagcca	tgactaggga	actgctcagg	720
gcccaagtac	catcttact	gggctccctc	ttaataaga	aggagaacaa	agaagttatt	780
cttaaacttc	tggtcatatt	tgagaacata	aatgataatt	tcaaatggga	agaaaatgaa	840
cctactcaga	atcaattcgg	tgaaggttca	ctttttctt	ttttaaaaga	atttcaagtg	900
tgtgctgata	agntctggg	aatagaaagt	caccatgatt	tttgggtgaa	agtaaaagtt	960
ggaaaattca	tggccaaact	tgctgaacat	atgttccaa	agagccagga	ataacacctt	1020
gattttgtaa	tttagaagca	acacacattt	taaactattt	attttctcca	cttgtttat	1080
atggtaaagg	aatccttca	gctgccagtt	ttgaataatg	aatatcatat	tgtatcatca	1140
atgctgatat	ttaactgagt	tggtctttag	gtttaagatg	gataaatgaa	tatcactact	1200
tgttctgaaa	acatgttgt	tgcttttat	ctcgctgcct	agattgaaat	attttgctat	1260
ttcttctggc	taaag					1275

<210> 9
 <211> 337
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> X=G, D, V, or A

<220>
 <221> misc_feature
 <222> (305)..(305)
 <223> Xaa can be any naturally occurring amino acid

<400> 9

Arg Gly Asp Val Asp Asp Ala Gly Asp Cys Ser Gly Ala Arg Tyr Asn
 1 5 10 15

Asp Trp Ser Asp Asp Asp Asp Ser Asn Glu Ser Lys Ser Ile Val
 20 25 30

Trp Tyr Pro Pro Trp Ala Arg Ile Gly Thr Glu Ala Gly Thr Arg Ala

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35

40

45

Arg Ala Arg Ala Arg Ala Arg Ala Thr Arg Ala Arg Arg Ala Val Gln
50 55 60

Lys Arg Ala Ser Pro Asn Ser Asp Asp Thr Val Leu Ser Pro Gln Glu
65 70 75 80

Leu Gln Lys Val Leu Cys Leu Val Glu Met Ser Glu Lys Pro Tyr Ile
85 90 95

Leu Glu Ala Ala Leu Ile Ala Leu Gly Asn Asn Ala Ala Tyr Ala Phe
100 105 110

Asn Arg Asp Ile Ile Arg Asp Leu Gly Gly Leu Pro Ile Val Ala Lys
115 120 125

Ile Leu Asn Thr Arg Asp Pro Ile Val Lys Glu Lys Ala Leu Ile Val
130 135 140

Leu Asn Asn Leu Ser Val Asn Ala Glu Asn Gln Arg Arg Leu Lys Val
145 150 155 160

Tyr Met Asn Gln Val Cys Asp Asp Thr Ile Thr Ser Arg Leu Asn Ser
165 170 175

Ser Val Gln Leu Ala Gly Leu Arg Leu Leu Thr Asn Met Thr Val Thr
180 185 190

Asn Glu Tyr Gln His Met Leu Ala Asn Ser Ile Ser Asp Phe Phe Arg
195 200 205

Leu Phe Ser Ala Gly Asn Glu Glu Thr Lys Leu Gln Val Leu Lys Leu
210 215 220

Leu Leu Asn Leu Ala Glu Asn Pro Ala Met Thr Arg Glu Leu Leu Arg
225 230 235 240

Ala Gln Val Pro Ser Ser Leu Gly Ser Leu Phe Asn Lys Lys Glu Asn
245 250 255

Lys Glu Val Ile Leu Lys Leu Leu Val Ile Phe Glu Asn Ile Asn Asp
260 265 270

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Asn Phe Lys Trp Glu Glu Asn Glu Pro Thr Gln Asn Gln Phe Gly Glu
275 280 285

Gly Ser Leu Phe Phe Leu Lys Glu Phe Gln Val Cys Ala Asp Lys
290 295 300

Xaa Leu Gly Ile Glu Ser His His Asp Phe Leu Val Lys Val Lys Val
305 310 315 320

Gly Lys Phe Met Ala Lys Leu Ala Glu His Met Phe Pro Lys Ser Gln
325 330 335

Glu

<210> 10
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Fragment of cytoplasmic domain of APP

<400> 10

Tyr Glu Asn Pro Thr Tyr
1 5

<210> 11
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fragment of SEQ ID NO:7

<400> 11

Asn Pro Ile Tyr
1